

SEQUENCE LISTING



<110> JENAPHARM GmbH & Co. KG

<120> Methods for Determining Hormonal Effects of Substances

<130> Pat 3684/11

<140> US/10/791,017

<141> 2004-03-02

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 2390

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44) .. (2011)

<223> EWS

<400> 1

agagggagac ggacgtttag	agaacgagga ggaaggagag	aaa atg gcg tcc acg	55
		Met Ala Ser Thr	
		1	

gat tac agt acc tat agc caa gct gca gcg cag cag ggc tac agt gct	103
Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Gln Gln Gly Tyr Ser Ala	
5 10 15 20	

tac acc gcc cag ccc act caa gga tat gca cag acc acc cag gca tat	151
Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr Thr Gln Ala Tyr	
25 30 35	

ggg caa caa agc tat gga acc tat gga cag ccc act gat gtc agc tat	199
Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr Asp Val Ser Tyr	
40 45 50	

acc cag gct cag acc act gca acc tat ggg cag acc gcc tat gca act	247
Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr Ala Tyr Ala Thr	
55 60 65	

tct tat gga cag cct ccc act ggt tat act act cca act gcc ccc cag	295
Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro Thr Ala Pro Gln	
70 75 80	

gca tac agc cag cct gtc cag ggg tat ggc act ggt gct tat gat acc	343
Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly Ala Tyr Asp Thr	
85 90 95 100	

acc act gct aca gtc acc acc cag gcc tcc tat gca gct cag tct	391		
Thr Thr Ala Thr Val Thr Thr Gln Ala Ser Tyr Ala Ala Gln Ser			
105	110	115	
gca tat ggc act cag cct gct tat cca gcc tat ggg cag cag cca gca	439		
Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly Gln Gln Pro Ala			
120	125	130	
gcc act gca cct aca aga ccg cag gat gga aac aag ccc act gag act	487		
Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys Pro Thr Glu Thr			
135	140	145	
agt caa cct caa tct agc aca ggg ggt tac aac cag ccc agc cta gga	535		
Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln Pro Ser Leu Gly			
150	155	160	
tat gga cag agt aac tac agt tat ccc cag gta cct ggg agc tac ccc	583		
Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro Gly Ser Tyr Pro			
165	170	175	180
atg cag cca gtc act gca cct cca tcc tac cct cct acc agc tat tcc	631		
Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro Thr Ser Tyr Ser			
185	190	195	
tct aca cag ccg act agt tat gat cag agc agt tac tct cag cag aac	679		
Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr Ser Gln Gln Asn			
200	205	210	
acc tat ggg caa ccg agc agc tat gga cag cag agt agc tat ggt caa	727		
Thr Tyr Gln Pro Ser Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln			
215	220	225	
caa agc agc tat ggg cag cag cct ccc act agt tac cca ccc caa act	775		
Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr Pro Pro Gln Thr			
230	235	240	
gga tcc tac agc caa gct cca agt caa tat agc caa cag agc agc agc	823		
Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln Gln Ser Ser Ser			
245	250	255	260
tac ggg cag cag agt tca ttc cga cag gac cac ccc agt agc atg ggt	871		
Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro Ser Ser Met Gly			
265	270	275	
gtt tat ggg cag gag tct gga gga ttt tcc gga cca gga gag aac cgg	919		
Val Tyr Gln Glu Ser Gly Gly Phe Ser Gly Pro Gly Glu Asn Arg			
280	285	290	
agc atg agt ggc cct gat aac cgg ggc agg gga aga ggg gga ttt gat	967		
Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg Gly Phe Asp			
295	300	305	
cgt gga ggc atg agc aga ggt ggg cgg gga gga cgc ggt gga atg	1015		
Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Arg Gly Gly Met			
310	315	320	

ggc agc gct gga gag cga ggt ggc ttc aat aag cct ggt gga ccc atg Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro Gly Gly Pro Met 325 330 335 340	1063
gat gaa gga cca gat ctt gat cta ggc cca cct gta gat cca gat gaa Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val Asp Pro Asp Glu 345 350 355	1111
gac tct gac aac agt gca att tat gta caa gga tta aat gac agt gtg Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu Asn Asp Ser Val 360 365 370	1159
act cta gat gat ctg gca gac ttc ttt aag cag tgt ggg gtt gtt aag Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys Gly Val Val Lys 375 380 385	1207
atg aac aag aga act ggg caa ccc atg atc cac atc tac ctg gac aag Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile Tyr Leu Asp Lys 390 395 400	1255
gaa aca gga aag ccc aaa ggc gat gcc aca gtg tcc tat gaa gac cca Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser Tyr Glu Asp Pro 405 410 415 420	1303
ccc act gcc aag gct gcc gtg gaa tgg ttt gat ggg aaa gat ttt caa Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly Lys Asp Phe Gln 425 430 435	1351
ggg agc aaa ctt aaa gtc tcc ctt gct cgg aag aag cct cca atg aac Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys Pro Pro Met Asn 440 445 450	1399
agt atg cgg ggt ggt ctg cca ccc cgt gag ggc aga ggc atg cca cca Ser Met Arg Gly Leu Pro Pro Arg Glu Gly Arg Gly Met Pro Pro 455 460 465	1447
cca ctc cgt gga ggt cca gga ggc cca gga ggt cct ggg gga ccc atg Pro Leu Arg Gly Gly Pro Gly Pro Gly Gly Pro Gly Gly Pro Met 470 475 480	1495
ggt cgc atg gga ggc cgt gga gga gat aga gga ggc ttc cct cca aga Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly Phe Pro Pro Arg 485 490 495 500	1543
gga ccc cgg ggt tcc cga ggg aac ccc tct gga gga gga aac gtc cag Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly Asn Val Gln 505 510 515	1591
cac cga gct gga gac tgg cag tgt ccc aat ccg ggt tgt gga aac cag His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly Cys Gly Asn Gln 520 525 530	1639
aac ttc gcc tgg aga aca gag tgc aac cag tgt aag gcc cca aag cct Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro 535 540 545	1687

gaa ggc ttc ctc ccg cca ccc ttt ccg ccc ccg ggt ggt gat cgt ggc	1735
Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly Gly Asp Arg Gly	
550 555 560	
aga ggt ggc cct ggt ggc atg cgg gga gga aga ggt ggc ctc atg gat	1783
Arg Gly Gly Pro Gly Gly Met Arg Gly Arg Gly Gly Leu Met Asp	
565 570 575 580	
cgt ggt ggt ccc ggt gga atg ttc aga ggt ggc cgt ggt gga gac aga	1831
Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Arg Gly Asp Arg	
585 590 595	
ggt ggc ttc cgt ggt ggc cgg ggc atg gac cga ggt ggc ttt ggt gga	1879
Gly Gly Phe Arg Gly Arg Gly Met Asp Arg Gly Phe Gly Gly	
600 605 610	
gga aga cga ggt ggc cct ggg ggg ccc cct gga cct ttg atg gaa cag	1927
Gly Arg Arg Gly Gly Pro Gly Pro Pro Gly Pro Leu Met Glu Gln	
615 620 625	
atg gga gga aga aga gga gga cgt gga gga cct gga aaa atg gat aaa	1975
Met Gly Gly Arg Arg Gly Arg Gly Pro Gly Lys Met Asp Lys	
630 635 640	
ggc gag cac cgt cag gag cgc aga gat cgg ccc tac tagatgcaga	2021
Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr	
645 650 655	
gaccccgca agctgcattt actaccagat ttatttttt aaccagaaaa tgttttaaat	2081
ttataattcc atatttataa tgttggccac aacattatga ttattccttgc tctgtacttt	2141
agtattttc accatttgtg aagaaacatt aaaacaagtt aaatggtagt gtgcggagtt	2201
ttttttctt ccttcttttta aaaatggttt ttaagactt taacaatggg aacccttgc	2261
gagcatgctc agtatcatttggagaacca agagggccctc ttaactgtaa caatgttcat	2321
ggttgtatg ttttttttttttttttaaaaatccaaatgtttaaataaaaaaaaaaaaaaa	2381
aa	2390

<210> 2
 <211> 656
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ala Ser Thr Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln	
1 5 10 15	
Gly Tyr Ser Ala Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr	
20 25 30	

Thr Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr
 35 40 45

Asp Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr
 50 55 60

Ala Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro
 65 70 75 80

Thr Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly
 85 90 95

Ala Tyr Asp Thr Thr Ala Thr Val Thr Thr Gln Ala Ser Tyr
 100 105 110

Ala Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly
 115 120 125

Gln Gln Pro Ala Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys
 130 135 140

Pro Thr Glu Thr Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln
 145 150 155 160

Pro Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro
 165 170 175

Gly Ser Tyr Pro Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro
 180 185 190

Thr Ser Tyr Ser Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr
 195 200 205

Ser Gln Gln Asn Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser
 210 215 220

Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr
 225 230 235 240

Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln
 245 250 255

Gln Ser Ser Ser Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro
 260 265 270

Ser Ser Met Gly Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro
 275 280 285

Gly Glu Asn Arg Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg
 290 295 300

Gly Gly Phe Asp Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly
 305 310 315 320

Arg Gly Gly Met Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro
 325 330 335

Gly Gly Pro Met Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val
340 345 350

Asp Pro Asp Glu Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu
355 360 365

Asn Asp Ser Val Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys
370 375 380

Gly Val Val Lys Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile
385 390 395 400

Tyr Leu Asp Lys Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser
405 410 415

Tyr Glu Asp Pro Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly
420 425 430

Lys Asp Phe Gln Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys
435 440 445

Pro Pro Met Asn Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg
450 455 460

Gly Met Pro Pro Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Pro
465 470 475 480

Gly Gly Pro Met Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly
485 490 495

Phe Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly
500 505 510

Gly Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly
515 520 525

Cys Gly Asn Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys
530 535 540

Ala Pro Lys Pro Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly
545 550 555 560

Gly Asp Arg Gly Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly
565 570 575

Gly Leu Met Asp Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg
580 585 590

Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly
595 600 605

Gly Phe Gly Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro
610 615 620

Leu Met Glu Gln Met Gly Gly Arg Arg Gly Gly Arg Gly Pro Gly
625 630 635 640

Lys Met Asp Lys Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
645 650 655

<210> 3
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 3
gattacgcta gcttgggtgg 20

<210> 4
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 4
gttgaagtga acttggcgaa g 21

<210> 5
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 5
gggtcgacgg acgttgagag aacgagg 27

<210> 6
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 6
ggaaattctg cggggtctct gcatctagta ggg 33

<210> 7
<211> 18
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 7
gcttgggtgg tcatatgg 18

<210> 8
<211> 918
<212> PRT
<213> Homo sapiens

<400> 8

Met	Glu	Val	Gln	Leu	Gly	Leu	Gly	Arg	Val	Tyr	Pro	Arg	Pro	Pro	Ser
1				5					10				15		
Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu
		20						25					30		
Val	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Ser	Ala	Ala
		35					40					45			
Pro	Pro	Gly	Ala	Ser	Leu	Leu	Leu	Gln							
	50				55				60						
Gln	Glu	Thr	Ser	Pro	Arg	Gln									
	65				70				75				80		
Gln	Gln	Gln	Gln	Gln	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Arg	Arg	
		85				90						95			
Gly	Pro	Thr	Gly	Tyr	Leu	Val	Leu	Asp	Glu	Glu	Gln	Gln	Pro	Ser	Gln
		100				105						110			
Pro	Gln	Ser	Ala	Leu	Glu	Cys	His	Pro	Glu	Arg	Gly	Cys	Val	Pro	Glu
		115					120					125			
Pro	Gly	Ala	Ala	Val	Ala	Ala	Ser	Lys	Gly	Leu	Pro	Gln	Gln	Leu	Pro
		130				135					140				
Ala	Pro	Pro	Asp	Glu	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser	Leu
	145				150					155			160		
Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Leu	Lys
		165				170						175			
Asp	Ile	Leu	Ser	Glu	Ala	Ser	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln	
		180				185						190			

Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg Ala Arg Glu Ala
 195 200 205
 Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu Gly Gly Thr Ser
 210 215 220
 Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser
 225 230 235 240
 Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln
 245 250 255
 Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly Val Pro Pro Ala
 260 265 270
 Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly Ser Leu
 275 280 285
 Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr Ala Glu Tyr Ser
 290 295 300
 Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly Glu Ser Leu Gly
 305 310 315 320
 Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr Leu Glu Leu Pro
 325 330 335
 Ser Thr Leu Ser Ley Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala
 340 345 350
 Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ala Gly Pro
 355 360 365
 Pro Pro Pro Pro Pro Pro His Pro His Ala Arg Ile Lys Leu Glu
 370 375 380
 Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Gln Cys
 385 390 395 400
 Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly Ala Ala Gly Pro
 405 410 415
 Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser Trp His Thr Leu
 420 425 430
 Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys Gly Gly Gly
 435 440 445
 Gly
 450 455 460
 Gly Gly Gly Gly Gly Glu Ala Glu Ala Val Ala Pro Tyr Gly
 465 470 475 480
 Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe Thr
 485 490 495

Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro Tyr
 500 505 510
 Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp Ser
 515 520 525
 Tyr Ser Gly Pro Tyr Gly Asp Met Arg Ley Glu Thr Ala Arg Asp His
 530 535 540
 Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile
 545 550 555 560
 Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly
 565 570 575
 Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr
 580 585 590
 Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys
 595 600 605
 Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr
 610 615 620
 Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu
 625 630 635 640
 Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr Gln
 645 650 655
 Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe
 660 665 670
 Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His
 675 680 685
 Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn
 690 695 700
 Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala
 705 710 715 720
 Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile
 725 730 735
 Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser
 740 745 750
 Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val
 755 760 765
 Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val
 770 775 780
 Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro
 785 790 795 800

Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro
805 810 815

Val Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Met Asn
820 825 830

Tyr Ile Lys Leu Glu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro
835 840 845

Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser
850 855 860

Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu
865 870 875 880

Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu
885 890 895

Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro
897 900 905 910

Ile Tyr Phe His Thr Gln
915